



THE UNITED STATES PATENT AND TRADEMARK OFFICE

**In re Application of:**

Boot et al.

Serial No.: 10/046,671

Filed: January 14, 2002

For: MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES

Examiner: To be assigned

Group Art Unit: 1642

Attorney Docket No.: 2183-5238US

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Serial No.: 10/046,671

3. The SEQUENCE LISTING submitted herewith is believed to contain no "new matter" with regard to the referenced patent application.

Respectfully submitted,



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Date: April 25, 2002

ACT/TLW/sw



3

SEQUENCE LISTING

<110> ~~TRADE~~ Hendrik J.  
Huurne ter, Anna A.H.M  
Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671  
<141> 2002-01-14

<150> PCT/NL00/00493  
<151> 2000-07-13

<150> EP 99202316.8  
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 TKSM and HK46

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Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
 35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
 50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
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Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
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Gly Asp Gln Met Ser Trp Ser  
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Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu  
35 40 45

Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
50 55 60

Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
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Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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20 25 30

Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr

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55

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Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
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Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
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Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
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Gly Asp Gln Met Ser Trp Ser  
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Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile  
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Gly Asp Gln Met Ser Trp Ser  
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<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 68

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate TKSMT

<400> 68

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 69

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate HK46-NT

<400> 69

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 70

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1)..(3260)

<223> Consensus cDNA sequence of IBDV A-segment

<400> 70

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cagatggaa ctcctccttc tacaaygcta tcattgtatgg tyagtagaga tcagacaaac 120  
gatcgacgatcg atgacraacc tgcaagatca aacccaaacag attgttccgt tcatacgag 180  
ccttctgatg ccaacaaccg gaccggcggtc cattccggac gacaccctrq agaagcacac 240  
tctcaggatca gagacctcga cctacaattt gactgtgggg gacacagggc cagggctaat 300  
tgtcttttc cctggwttcc ctggctcaat tgtgggtgct cactacacac tgcagagcaa 360  
tggaaactac aagttcgatc agatgctcct gactgcccag aacctaccgg ccagytacaa 420  
ctactgcagg ctatgtgatc ggagtctcac agtgaggatca agcacactyc ctggtggcgt 480  
ttatgcacta aayggcacca taaacgcccgt gaccttccaa ggaagcctga gtgaactgac 540

agatgttagc tacaatgggt ttagtgcatac aacagccaac atcaacgaca aaatyggaa 600  
 cgtcctagta ggggaagggg tmaccgtcct cagcttaccc acatcatatg atcttggta 660  
 tgtgagrcty ggtgacccca ttcccgwat agggctygcac caaaaaatgg tagcmacatg 720  
 tgacagcagt gacaggccca gagtctacac cataactgca gccgatgatt accaattctc 780  
 atcacagtac caascaggtg gggtaacaat cacactgttc tcagcyaaya tygatgccat 840  
 cacaaggcctc agcrttyggg gagarctcggtttcaaaca agcgtccamg gcctrrtact 900  
 ggggcyacc atctacctya taggcttga tggacwgcg gtaatcacca grgctgtggc 960  
 cgaracaat gggctracgr cccgcacyga caaccttwtg ccattcaatm ttgtgattcc 1020  
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 tgggtgtcag gcrggggatc agatgtcrtg gtcrgcaagw gggagcctag cagtgacgat 1140  
 ccaygggtggc aactatccag gggccctccg tcccgtcacr cttagtrgcct acgaaagagt 1200  
 gcaacacagga tcygtcgta cggtcgcygg ggtgagcaac ttcgagctga tcccaaatcc 1260  
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 cacaaaaattg atactgagtg agagggacccg tcttgcattc aagaccgtmt ggccaacaag 1380  
 ggagtacact gactttcgyg artacttcat ggaggtggcc gacctaact ctcccctgaa 1440  
 gattgcagga gcattyggct tcaaagacat aatccgggccc mtaaggagga tagctgtgcc 1500  
 ggtggtctcy acaytggcc caccyggccg tcccctagcc catgaattt gggaggtgt 1560  
 agactacctg ctggggcgtg aggacacaggg tgcttcagga actgctcgag cgcgtcagg 1620  
 aaaagcaaga gctgcctcag gcccataag gcagctract ctcgcgcggc acaagggta 1680  
 cgaggttagtc gcgaatctrtycaggtgcc ccagaatccy gtagtcgacg ggattctygc 1740  
 ttcacctggg rtactcccggygcacacaa cctcgaactgc gtgttragag aggggtccac 1800  
 gctattccct gtggtyatya cgacagtggaa agayggcatg acacccaaag caytgaacag 1860  
 caaaatgttt gctgtcattt aaggcgtcgagaagayctcaaacctccwt ctcaaagagg 1920  
 atccttcata cgaactctct cyggacayag agtctatggatatgctccag atgggtact 1980  
 tccactggag actgggagag aytacaccgt kgtcccaata gatgatgtct gggacgacag 2040  
 cattatgctg tccaaagayccataccctcc tattgtggaa aacagyygaa ayctagccat 2100  
 agcttacatg gatgtgttccgacccaaagt cccmatccat gtggcyatga cgggagccct 2160  
 caaygcyytgcgaggattt agaamgtracccatgatgatgttccatgatgatgtct gcaactgcaca 2220  
 ccgacttggc ctyaaggcttgg ctggcccg wgcattygatgatgatgttccatgatgatgtct 2280  
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 mgagttcaaa gagaccccmg aactcgarr ygcgtsgmw gcmatggamg cwgcwgcmaa 2460  
 cgtsgaccca ytrttccrmt cgcdctcmr bgtsttcatg tgggtggaa araaayggat 2520  
 tgtracygay atggcyaact tcgcmtcag cgaccgaac gcmcaymgga tgmrmaattt 2580  
 ycthgcaaay gcwccmcarg cmggmagca gtcgcaragr gccaagtagt gsaacrgcwgg 2640  
 ctacggagtg gaggcymrg gccccacdcc agargargca cagagggara aagacacacg 2700  
 gatctcmaag aagatggara cbatggcat ctacttygca acaccrgaat ggtagcact 2760  
 caaygggcac cgrggsccaa gccccggcca gctvaagtac tggcaraaca camgagaaat 2820  
 accdgahccm aacgaggact aycyagacta ygtgcaygcr gagaagagcc ggttggcrtc 2880  
 agaagaacar rtytaaggg cagcyacgatc gatctacggg gctccaggac aggwgarc 2940  
 accccaagcy ttcatagacg aagtygccc rgtctatgaa atcaaccatg grcgtggyc 3000  
 maaccargar cagatgaarg ayctgctcyt gactgcgtatg gagaatgac atcgcataatcc 3060  
 caggcgggct cyaccaaagc cmaagccaaa acccaatgct ccawcacaga gacccttgg 3120  
 wcgctgggc cgctggatca ggrcgbtctc tgaygaggac ytkgagttag gywctggga 3180  
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 gatccgttc gcggtcccc 3260

<210> 71  
 <211> 3260  
 <212> DNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_feature

<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBDV A-segment

<400> 71

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caggatggaa ctcctccttc tacaacgcta tcattgtatgg tcagtagaga tcagacaaac 120  
gatccgcagcg atgacaaacc tgcaagatca aacccaacag attgttccgt tcatacggag 180  
ccttctgtatg ccaacaaccg gaccggcgtc cattccggac gacaccctgg agaagcacac 240  
tctcaggatca gagacctcga cctacaattt gactgtgggg gacacaggtt caggctaat 300  
tgtcttttc cctggattcc ctggctcaat tgtgggtct cactacacac tgcagagcaa 360  
tgggaactac aagttcgatc agatgctcct gactgcccag aacctaccgg ccagttacaa 420  
ctactgcagg ctagtgatc ggagtctcac agtgaggtca agcacacttc ctggggcgt 480  
ttatgcacta aacggcacca taaacgcccgt gacctccaa ggaaggctga gtgaactgac 540  
agatgttagc tacaatgggt ttagtgcatac aacagccaac atcaacgaca aaattggaa 600  
cgcccttagta ggggaagggg tcaccgtcct cagcttaccc acatcatatg atcttggta 660  
tgtgaggctt ggtgacccca tttccgcaat agggcttgc caaaaatgg tagccacatg 720  
tgacagcgt gacaggccca gagtctacac cataactgca gccgatgatt accaattctc 780  
atcacagtagc caaccaggatg ggttaacaat cacactgtt tcagccaaca ttgatgccat 840  
cacaaggctc agcggtgggg gagagctcgt gtttcaaaca agcggtccacg gccttgtact 900  
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aacmarcgag ataaccaggc caatcacatc catcaaactg gagatagtga cctccaaaag 1080  
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cgtggaccca ctattccat ctgcactcgat tggctcatg tggctggaa agaatggat 2520  
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agaagaacaa atcctaaggg cagctacgtc gatctacggg gtcggaggac aggcagagcc 2940  
accccaagct ttcatacgacg aagttgccaat agtctatgaa atcaaccatg gacgtggccc 3000  
aaaccaagaa cagatgaaatg atctgcttgc gactgctatc gatgaaatcc 3060

caggcgggct ctaccaaagc ccaagccaaa acccaatgct ccaacacaga gacccctgg 3120  
tcgctgggc cgctggatca ggaccgtctc ttagtggag cttgagtgag gtacctggg 3180  
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ggatccgttc gcgggtcccc 3260

<210> 72  
<211> 3260  
<212> DNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_feature  
<222> (1)..(3260)  
<223> cDNA sequence D6948-A of IBDV A-segment

<400> 72  
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gatcgcagcg atgacgaacc tgcaagatca aacccaaacag attgttccgt tcatacggag 180  
ccttctgatg ccaacaaccg gaccggcgctc cattccggac gacaccctag agaagcacac 240  
tctcaggtca gagacctcga cctacaattt gactgtgggg gacacagggt cagggcta 300  
tgtcttttc cctgggttcc ctggctcaat tgtgggtgct cactacacac tgcagagcaa 360  
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cgtcctagta ggggaagggg taaccgtcct cagcttaccc acatcatatg atcttggta 660  
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tgacagcagt gacaggccca gagtctacac cataactgca gccgatgatt accaattctc 780  
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ggagtacact gactttcgctg agtacttcat ggaggtggcc gacctcaact ctccctgaa 1440  
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cgaggttagtc gcgaatctgt ttcaagggtgc ccagaatctt gtatgcacg ggattctcgc 1740  
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cgtggaccca ctgttccaaat ctgcgtcaga cgtgtcatg tggctggaa agaatggat 2520  
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agaagaacaa atcctaaggg cagctacgtc gatctacggg gtcaggac aggcaagagcc 2940  
accccaagcc ttcatagacg aagtgcggaa agtctatgaa atcaaccatg ggcgtggccc 3000  
caaccaagaa cagatgaaag atctgctcct gactgcgtatc gagatgaagc atcgcaatcc 3060  
caggcgggct ccaccaaaagc ccaagccaaa acccaatgtc ccaacacaga gaccggctgg 3120  
tcggctgggc cgctggatca ggctgtctc tcatgaggac cttgagttag gtacctggga 3180  
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ggatccgttc gcgggtcccc 3260

<210> 73  
<211> 964  
<212> DNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_feature  
<222> (1)..(964)  
<223> cDNA sequence TY89-A of IBDV A-segment

<400> 73  
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ccaccaacag ctggacgtca gttccatctg gcccctggcag cctccgagtt caaagagacc 120  
ccagaactcg aagacgtgt gctgtcaatg gacgtgtctg caaacgtcga cccattgttc 180  
cgctcagctc tccaggctt catgtgggtt gaagaaaaacg ggattgtac cgacatggct 240  
aacattcgccc tcagcgaccc gaacgcacac aggtaaaaa atttccttagc aaatgctccc 300  
caggccggaa gcaagtcgca gaggggcaag tatggcacgg ctggctacgg agtggaggct 360  
agaggccccca cgccagaaga ggcacagagg gagaaagaca cacggatctc caagaagatg 420  
gaaacgatgg gcatctactt cgcaacacccg gaatgggtag cactcaacgg gcaccgaggc 480  
ccaagccccg gccagctcaa gtactggcaa aacacaagag aaataccaga acccaacgag 540  
gactacccag actatgtcga cgcggagaag agccgggttgg cgtcagaaga acaggtctt 600  
agggcagcca cgtcgatcta cggggctcca ggacaggctg aaccacccca agccttcata 660  
gacaagtcg ccagggtcta tggaaatcaac catgggtgt gtcaccaacca ggagcagatg 720  
aaggacctgc tcctgactgc gatggagatg aagcatcgca atcccaggcg ggctccacca 780  
aagccaaagc caaaacccaa tgctccatca cagagacccc ctggacggct gggccgctgg 840  
atcaggacgg tctctgacga ggacttggag tgaggctcct gggagtctcc cgacaccacc 900  
cgccgcagggtg tggacaccaa ttaatacta gtgaattcga aattggatcc gttcgccgggt 960  
cccc 964

<210> 74  
<211> 2827  
<212> DNA  
<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1) .. (2827)

<223> Consensus cDNA sequence of IBDV B-segment

<400> 74

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rttttcaaya gtcacaggc gcaagcamg atmtcagcag cgttccgat aaagcctacw 180  
gctggacarg aytggaaaga actcytgatc cctaargtyt gggtgccacc tgaggatccs 240  
ytkgccagcc ctatcgwct ggcmaagtcc ctcagrgara acggctacaa rrttytgag 300  
ccacggctc trccyagaa tgaggagtt gagaccgacy aaatactccc wgacytagcw 360  
tggatgmrc agatagargg rgctgttta aaaccmacyc tatctctccc yattggagay 420  
caggagtaact tcccwaarta ctacccaaca caycggccka gcaaggaraa gcccaatgcf 480  
tacccgcmg ayatcgayt actcaagcag atgatytacy tgtttctcca gtttccmagg 540  
gccammgakr rcctwaarga tgargtmacc ctmytraccc aaaacatwag rgayaargcc 600  
tayggragtg ggacctacat ggacargcm acymgacttg tkgyatgaa rgaggtgccc 660  
actggragaa acccaaacaa rgatccctca aagctgggt acacyttga gagcatmgcs 720  
cagctactg acatcacwyt accggtaggc ccacccgggt aggatgacaa gcccctgggr 780  
ccactcacaa grgtggcgtc amggatgtt gtwctgacgg gmgacgtaga tggsgamtt 840  
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cttctcgag caggracgag cagaccaatg gggatggagg cyccaaacacg gtccaagaac 2700  
gccgtaaaaa tggccaaamg gcccacacg caaaargaga gcccggaaaya gccatgtatgg 2760  
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ggccccc 2827

<210> 75  
<211> 2827  
<212> DNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_feature  
<222> (1)..(2827)  
<223> cDNA sequence CEF94-B of IBDV B-segment

<400> 75  
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atttcaaca gtccacaggc gcgaagcagc atctcagcag cgttcggcat aaaggctact 180  
gctggacaag acgtggaaga actcttgatc cctaaagtt ggggccacc tgaggatccg 240  
cttgcgcagcc ctagtcgact ggcaaaagttc ctcagagaga acggctacaa agtttgcag 300  
ccacggtctc tgcccagaa tgaggatgt gagaccgacc aaatactccc agacttagca 360  
tggatgcgac agatagaagg ggctgttta aaaccactc tatctctccc tattggagat 420  
caggagact tcccaaagta ctacccaaca catgcctca gcaaggagaa gcccaatgcg 480  
taccgcctc acatcgact actcaagcag atgatttacc tgtttctcca gtttccagag 540  
gcacaacgagg gcctaaagga tgaagtaacc ctcttgaccc aaaacataag ggacaaggcc 600  
tatggaagtg ggacctacat ggacaagca actcgactt gggccatgaa ggaggtcgcc 660  
actggaagaa acccaaacaa ggatcctcta aagctgggt acactttga gacatcgcg 720  
cagctacttg acatcacact accggtaggc ccacccggtg aggtgacaa gccctgggtg 780  
ccactcacaa gagtgccgtc acggatgtt gtaactgacgg gagacgtaga tggcacttt 840  
gaggtgaag attaccccttcc caaaatcaac ctcaagtcat caagtggact accatatgt 900  
ggtcgcacca aaggagagac aattggcgag atgatagcta tctcaaaccg 960  
gagctatcaa cactgtgaa gcaaggtgca gggacaaagg ggtcaaacaa gaagaagcta 1020  
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ttgaacattt aagggtgtcc atcactctac aaattcaacc cgttcagagg agggttgaac 1260  
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tgcaactcgcc aacacatgca agccgcaatg tactacatac tcaccagagg gtggcagac 1440  
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tggaacctga tgagacagcc cagaccagac agcgaggagt tcaaatcaat tgaggacaag 1680  
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tccaaaccccg ttgttggctt ccacctgcccc gccaagagag ccaccgggtt ccaggccgt 2640

cttctcgag caggaacgag cagaccaatg gggatggagg ccccaacacg gtccaagaac 2700  
gccgtaaaa tggccaaacg gcccacgc caaaaggaga gcccacaaca gccatgatgg 2760  
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ggccccc 2827

<210> 76  
<211> 2827  
<212> DNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_feature  
<222> (1)..(2827)  
<223> cDNA sequence D6948-B of IBDV B-segment

<400> 76  
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gttttcaata gtccacaggc gcaagcaag atatcagcag cgttcggcat aaaggctaca 180  
gctggacagg atgtgaaaga actcctgatc cctaaggtct ggggtgccacc tgaggatccc 240  
ttggccagcc ctatgtcgtt gccaagttc ctcaggaaa acggctacaa gattctgcag 300  
ccacggcttc tacctgagaa tgaggagtt gagaccgatc aaatactccc tgacctagct 360  
tggatgaggg agatagaggg agctgtttta aaaccaaccc tatctctccc cattggagac 420  
caggagttact tccctaaata ctacccaaca caccggccga gcaaggaaaa gcccaatgcg 480  
tacccgcccg atatgcatt actcaagcag atgatctact tgtttctcca ggttcccgag 540  
gccccacagata accttaaaga tgaggtcacc ctactaaccc aaaacattag agataaagcc 600  
tacgggagtg ggacctacat ggacaggcc accagactt gttcttatgaa agaggttgcc 660  
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cagctactt acatcaactt accggtaggc ccacccgggtg aggtgacaa gcccotggta 780  
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ggccccc 2827

<210> 77  
<211> 1012  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(1012)  
<223> Consensus sequence of IBDV polyprotein, whereby the Xaa  
indicator may be any amino acid

<400> 77  
Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
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Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
100 105 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
115 120 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
145 150 155 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly

165	170	175
Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys		
180	185	190
Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile		
195	200	205
Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Xaa Gly Gly		
210	215	220
Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu		
225	230	235
240		
Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa		
245	250	255
Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile		
260	265	270
Thr Arg Ala Val Ala Ala Xaa Asn Gly Leu Thr Xaa Gly Thr Asp Asn		
275	280	285
Leu Xaa Pro Phe Asn Xaa Val Ile Pro Thr Xaa Glu Ile Thr Gln Pro		
290	295	300
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln		
305	310	315
320		
Ala Gly Asp Gln Met Ser Trp Ser Ala Xaa Gly Ser Leu Ala Val Thr		
325	330	335
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val		
340	345	350
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val		
355	360	365
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val		
370	375	380
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu		
385	390	395
400		
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr		
405	410	415
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu		
420	425	430
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile		
435	440	445
Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro		
450	455	460

Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640  
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735  
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750

Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765  
 Val Arg Ala Met Glu Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780  
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800  
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815  
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu  
 835 840 845  
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr  
 850 855 860  
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His  
 865 870 875 880  
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu  
 885 890 895  
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys  
 900 905 910  
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile  
 915 920 925  
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
 930 935 940  
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
 945 950 955 960  
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
 965 970 975  
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
 980 985 990  
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp  
 995 1000 1005  
 Glu Asp Leu Glu  
 1010

<210> 78  
 <211> 1012  
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(1012)

<223> Sequence of IBDV polyprotein CEF94-PP

<400> 78

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
1 5 10 15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
100 105 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
115 120 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
145 150 155 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
165 170 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
180 185 190

Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
210 215 220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
225 230 235 240

Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val  
245 250 255

Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Leu Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr  
 325 330 335  
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430  
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly  
 530 535 540

Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640  
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735  
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750  
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765  
 Val Arg Ala Met Glu Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780  
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800  
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815  
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu

835	840	845
Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr		
850	855	860
Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His		
865	870	880
Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu		
885	890	895
Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys		
900	905	910
Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile		
915	920	925
Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu		
930	935	940
Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu		
945	950	955
Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn		
965	970	975
Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr		
980	985	990
Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp		
995	1000	1005
Glu Asp Leu Glu		
1010		

<210> 79  
 <211> 1012  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(1012)  
 <223> Sequence of IBDV polyprotein D6948-PP

<400> 79  
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
 1 5 10 15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
 20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
 35 40 45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
 50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
 65 70 75 80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
 85 90 95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
 100 105 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
 115 120 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
 130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145 150 155 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
 165 170 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
 180 185 190

Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
 195 200 205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly  
 210 215 220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
 225 230 235 240

Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile  
 245 250 255

Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile  
 260 265 270

Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn  
 275 280 285

Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro  
 290 295 300

Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320

Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr  
 325 330 335

Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430  
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu

625	630	635	640
Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala			
645	650	655	
Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala			
660	665	670	
Met Thr Gly Ala Leu Asn Ala Tyr Gly Glu Ile Glu Asn Val Ser Phe			
675	680	685	
Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala			
690	695	700	
Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Ser Asn Trp Ala Thr Phe			
705	710	715	720
Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr			
725	730	735	
Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr Asp Leu			
740	745	750	
Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala			
755	760	765	
Val Arg Ala Met Glu Ala Ala Asn Val Asp Pro Leu Phe Gln Ser			
770	775	780	
Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp			
785	790	795	800
Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn			
805	810	815	
Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys			
820	825	830	
Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu			
835	840	845	
Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr			
850	855	860	
Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His			
865	870	875	880
Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu			
885	890	895	
Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys			
900	905	910	
Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile			
915	920	925	

Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
930 935 940

Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
945 950 955 960

Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
965 970 975

Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
980 985 990

Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Ala Val Ser Asp  
995 1000 1005

Glu Asp Leu Glu  
1010

<210> 80

<211> 290

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(290)

<223> Sequence of IBDV polyprotein TY89-PP

<400> 80

Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn  
1 5 10 15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu  
20 25 30

Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg  
35 40 45

Ala Met Asp Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu  
50 55 60

Gln Val Phe Met Trp Leu Glu Asn Gly Ile Val Thr Asp Met Ala  
65 70 75 80

Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu  
85 90 95

Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly  
100 105 110

Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala  
115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly  
130 135 140

Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly  
145 150 155 160

Pro Ser Pro Gly Gln' Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro  
165 170 175

Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg  
180 185 190

Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly  
195 200 205

Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala  
210 215 220

Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met  
225 230 235 240

Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg  
245 250 255

Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg  
260 265 270

Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp  
275 280 285

Leu Glu  
290

<210> 81  
<211> 881  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(881)  
<223> Consensus sequence of IBDV VP1, whereby the Xaa  
indicator may be any amino acid

<400> 81  
Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala  
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Xaa Leu Gln Pro  
 50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
 65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
 85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
 100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
 115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
 130 135 140

Xaa Xaa Xaa Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
 145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
 165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
 180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240

Gly Xaa Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255

Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270

Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Xaa Leu  
 275 280 285

Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300

Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320

Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335

Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr

340	345	350
Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly		
355	360	365
Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg		
370	375	380
Ile Val Glu Trp Ile Xaa Ala Pro Xaa Glu Pro Lys Ala Leu Val Tyr		
385	390	395
Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp		
405	410	415
Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala		
420	425	430
Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met		
435	440	445
Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu		
450	455	460
Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr		
465	470	475
Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu		
485	490	495
Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Xaa Gln Pro Xaa Pro		
500	505	510
Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe		
515	520	525
Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu		
530	535	540
Val Xaa Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu		
545	550	555
Gln Xaa Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr		
565	570	575
Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg		
580	585	590
Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu		
595	600	605
Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu		
610	615	620
Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala		
625	630	635
640		

Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
                   645                  650                  655  
  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
                   660                  665                  670  
  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu  
                   675                  680                  685  
  
 Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val  
                   690                  695                  700  
  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
                   705                  710                  720  
  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
                   725                  730                  735  
  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
                   740                  745                  750  
  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
                   755                  760                  765  
  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
                   770                  775                  780  
  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
                   785                  790                  800  
  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
                   805                  810                  815  
  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
                   820                  825                  830  
  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
                   835                  840                  845  
  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala  
                   850                  855                  860  
  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa  
                   865                  870                  880

Xaa

<210> 82  
 <211> 881  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala  
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro  
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
130 135 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
225 230 235 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
245 250 255

Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
260 265 270

Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320  
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335  
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr  
 340 345 350  
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly  
 355 360 365  
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg  
 370 375 380  
 Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr  
 385 390 395 400  
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp  
 405 410 415  
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala  
 420 425 430  
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met  
 435 440 445  
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu  
 450 455 460  
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr  
 465 470 475 480  
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu  
 485 490 495  
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro  
 500 505 510  
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe  
 515 520 525  
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu  
 530 535 540  
 Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu  
 545 550 555 560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr  
 565 570 575  
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg  
 580 585 590  
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu  
 595 600 605  
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu  
 610 615 620  
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala  
 625 630 635 640  
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu  
 675 680 685  
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val  
 690 695 700  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
 705 710 715 720  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
 725 730 735  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
 740 745 750  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
 755 760 765  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
 770 775 780  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
 820 825 830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
 835 840 845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala

850

855

860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln  
865 870 875 880

Pro

<210> 83

<211> 879

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)...(879)

<223> Sequence of IBDV D6948-VP1

<400> 83

Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala  
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro  
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
130 135 140

Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205  
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220 240  
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240  
 Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255  
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270  
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320  
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335  
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr  
 340 345 350  
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly  
 355 360 365  
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg  
 370 375 380  
 Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr  
 385 390 395 400  
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp  
 405 410 415  
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala  
 420 425 430  
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met  
 435 440 445  
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu  
 450 455 460  
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr  
 465 470 475 480  
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu

485	490	495
Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Lys Gln Pro Ser Pro		
500	505	510
Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe		
515	520	525
Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu		
530	535	540
Val Pro Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu		
545	550	555
Gln Pro Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr		
565	570	575
Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg		
580	585	590
Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu		
595	600	605
Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu		
610	615	620
Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala		
625	630	635
Cys Lys Asn Asn Ala Ser Ala Ala Arg Arg His Leu Glu Ala Lys Gly		
645	650	655
Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe		
660	665	670
Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Pro Glu		
675	680	685
Ser Leu Ala Glu Leu Asn Arg Pro Val Pro Pro Lys Pro Pro Asn Val		
690	695	700
Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu		
705	710	715
720		
Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu		
725	730	735
Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala		
740	745	750
Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp		
755	760	765
Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp		
770	775	780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala			
785	790	795	800
Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu			
805	810	815	
Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu			
820	825	830	
Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly			
835	840	845	
Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala			
850	855	860	
Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln			
865	870	875	

<210> 84			
<211> 145			
<212> PRT			
<213> Infectious bursal disease virus			
<220>			
<221> DOMAIN			
<222> (1)..(145)			
<223> Consensus sequence of IBDV VP5, whereby the Xaa			
indicator may be any amino acid			
<400> 84			
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala			
1	5	10	15
Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala			
20	25	30	
Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His			
35	40	45	
Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg			
50	55	60	
Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly			
65	70	75	80
Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp			
85	90	95	
Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Gln Ala			
100	105	110	
Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg			

115

120

125

Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
130 135 140

Glu  
145

<210> 85  
<211> 145  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(145)  
<223> Sequence of IBDV D6948-VP5

<400> 85  
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala  
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His  
35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly  
65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg  
115 120 125

Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
130 135 140

Glu  
145

<210> 86  
<211> 145  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(145)  
<223> Sequence of IBDV CEF94-VP5

<400> 86  
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala  
1 5 10 15  
Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
20 25 30  
Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His  
35 40 45  
Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
50 55 60  
Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly  
65 70 75 80  
Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
85 90 95  
Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Gln Ala  
100 105 110  
Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg  
115 120 125  
Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
130 135 140  
Glu  
145

<210> 87  
<211> 149  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(149)  
<223> Sequence of IBDV D6948-VP5

<400> 87  
Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp  
1 5 10 15  
Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu  
20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro  
35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys  
50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp  
65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln  
85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln  
100 105 110

Leu Leu Gln Ala Ser Glu Ser His Ser Glu Val Lys His Thr  
115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu  
130 135 140

Pro Arg Lys Pro Glu  
145